



Substitute Sequence Listing ascii txt.txt

<110> APPLICANT: TEDESCO, Francesco  
MARZARI, Roberto

<120> TITLE OF INVENTION: Antibodies anti C5 of the complement and their use

<130> FILE REFERENCE: 50294/016001

<140> CURRENT APPLICATION NUMBER: US/10/521,109

<141> CURRENT FILING DATE: 2005-01-11

<150> PRIOR APPLICATION NUMBER: PCT/EP2003/007487

<151> PRIOR FILING DATE: 2003-07-10

<150> PRIOR APPLICATION NUMBER: MI2002A001527

<151> PRIOR FILING DATE: 2002-07-11

<160> NUMBER OF SEQ ID NOS: 35

<170> SOFTWARE: PatentIn version 3.1

<210> SEQ ID NO 1

<211> LENGTH: 342

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(342)

<223> OTHER INFORMATION: Light chain of the TS-A12/22 antibody

<400> SEQUENCE: 1

gac atc cgg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc	48
Asp Ile Arg Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1 5 10 15	
gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20 25 30	
tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35 40 45	
cct cct aag ctg ctc att tac tgg gca tct acc cggtt gaa tcc ggg gtc	192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50 55 60	
cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65 70 75 80	
atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85 90 95	
tat tat agt act cct cag ctc act ttc ggc gga agg acc aaa gtg gat	336
Tyr Tyr Ser Thr Pro Gln Leu Thr Phe Gly Gly Arg Thr Lys Val Asp	
100 105 110	
atc aaa	342
Ile Lys	

<210> SEQ ID NO 2

<211> LENGTH: 114

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

Asp Ile Arg Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly

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1	5	10	15	
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	20	25	30	
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	35	40	45	
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	50	55	60	
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	65	70	75	80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	85	90	95	
Tyr Tyr Ser Thr Pro Gln Leu Thr Phe Gly Gly Arg Thr Lys Val Asp	100	105	110	
Ile Lys				

<210> SEQ ID NO 3  
<211> LENGTH: 345  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)..(345)  
<223> OTHER INFORMATION: Heavy chain of the TS-A12/22 antibody  
<400> SEQUENCE: 3

cag gta cag ctg cag cag tca gag gga ggc gtg gtc cag cct ggg agg	48
Gln Val Gln Leu Gln Gln Ser Glu Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt agc tat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20 25 30	
ggc atg aac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtt	144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
tca tac att agt agt agt agt agt acc ata tac tac gca gac tct gtg	192
Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val	
50 55 60	
aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aga ggg cct ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc	336
Ala Arg Gly Pro Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr	
100 105 110	
gtc tcc tca	345
Val Ser Ser	
115	

<210> SEQ ID NO 4  
<211> LENGTH: 115  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens  
<400> SEQUENCE: 4

Gln Val Gln Leu Gln Gln Ser Glu Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20 25 30	
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val	

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50	55	60													
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
									85	90				95	
Ala	Arg	Gly	Pro	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr
								100	105				110		
Val	Ser	Ser													
															115

<210> SEQ\_ID NO 5

<211> LENGTH: 750

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(750)

<223> OTHER INFORMATION: scFv

<400> SEQUENCE: 5

gac atc cgg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc	48
Asp Ile Arg Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1 5 10 15	
gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20 25 30	
tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35 40 45	
cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc	192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50 55 60	
cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65 70 75 80	
atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85 90 95	
tat tat agt act cct cag ctc act ttc ggc gga agg acc aaa gtg gat	336
Tyr Tyr Ser Thr Pro Gln Leu Thr Phe Gly Gly Arg Thr Lys Val Asp	
100 105 110	
atc aaa tcc gga ggg tcg acc ata act tcg tat aat gta tac tat acg	384
Ile Lys Ser Gly Gly Ser Thr Ile Thr Ser Tyr Asn Val Tyr Tyr Thr	
115 120 125	
aag tta tcc tcg agc ggt acc cag gta cag ctg cag cag tca gag gga	432
Lys Leu Ser Ser Ser Gly Thr Gln Val Gln Leu Gln Gln Ser Glu Gly	
130 135 140	
ggc gtc gtc cag cct ggg agg tcc ctg aga ctc tcc tgt gca gcg tct	480
Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser	
145 150 155 160	
gga ttc acc ttc agt agc tat ggc atg aac tgg gtc cgc cag gct cca	528
Gly Phe Thr Phe Ser Ser Tyr Gly Met Asn Trp Val Arg Gln Ala Pro	
165 170 175	
ggg aag ggg ctg gag tgg gtt tca tac att agt agt agt agt agt acc	576
Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr	
180 185 190	
ata tac tac gca gac tct gtg aag ggc cga ttc acc atc tcc aga gac	624
Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp	
195 200 205	
aat tcc aag aac acg ctg tat ctg caa atg aac agc ctg aga gcc gag	672
Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu	
210 215 220	
gac acg gct gtg tat tac tgt gcg aga ggg cct ggt atg gac gtc tgg	720

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Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Pro	Gly	Met	Asp	Val	Trp
225				230					235				240		
ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca						750
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser						
										245		250			

<210> SEQ ID NO 6  
<211> LENGTH: 250  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens  
<400> SEQUENCE: 6

Asp	Ile	Arg	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5				10						15	
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser
								20	25					30	
Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
								35	40				45		
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
								50	55				60		
Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr
	65			70					75					80	
Ile	Ser	Ser	Leu	Gln	Ala	Glu	Asp	Val	Ala	Val	Tyr	Tyr	Cys	Gln	Gln
								85	90				95		
Tyr	Tyr	Ser	Thr	Pro	Gln	Leu	Thr	Phe	Gly	Gly	Arg	Thr	Lys	Val	Asp
								100	105				110		
Ile	Lys	Ser	Gly	Gly	Ser	Thr	Ile	Thr	Ser	Tyr	Asn	Val	Tyr	Tyr	Thr
								115	120				125		
Lys	Leu	Ser	Ser	Ser	Gly	Thr	Gln	Val	Gln	Leu	Gln	Gln	Ser	Glu	Gly
								130	135				140		
Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser
	145				150				155					160	
Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro
								165	170				175		
Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Tyr	Ile	Ser	Ser	Ser	Ser	Thr	
								180	185				190		
Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp
								195	200				205		
Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu
								210	215				220		
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Pro	Gly	Met	Asp	Val	Trp
	225				230				235					240	
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser						
								245	250						

<210> SEQ ID NO 7  
<211> LENGTH: 15  
<212> TYPE: DNA  
<213> ORGANISM: homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)..(15)  
<223> OTHER INFORMATION: CDR1 region of VH  
<400> SEQUENCE: 7

agc	tat	ggc	atg	aac											15
			Ser	Tyr	Gly	Met	Asn								
1								5							

<210> SEQ ID NO 8  
<211> LENGTH: 5  
<212> TYPE: PRT

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<213> ORGANISM: homo sapiens  
<400> SEQUENCE: 8  
Ser Tyr Gly Met Asn  
1 . . . 5

<210> SEQ ID NO 9  
<211> LENGTH: 51  
<212> TYPE: DNA  
<213> ORGANISM: homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)..(51)  
<223> OTHER INFORMATION: CDR2 region of VH  
<400> SEQUENCE: 9  
tac att agt agt agt agt acc ata tac tac gca gac tct gtg aag  
Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys  
1 . . . 5 . . . 10 . . . 15  
ggc  
Gly

48  
51

<210> SEQ ID NO 10  
<211> LENGTH: 17  
<212> TYPE: PRT  
<213> ORGANISM: homo sapiens  
<400> SEQUENCE: 10  
Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys  
1 . . . 5 . . . 10 . . . 15  
Gly

<210> SEQ ID NO 11  
<211> LENGTH: 18  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)..(18)  
<223> OTHER INFORMATION: CDR3 region of VH  
<400> SEQUENCE: 11  
ggg cct ggt atg gac gtc  
Gly Pro Gly Met Asp Val  
1 . . . 5

18

<210> SEQ ID NO 12  
<211> LENGTH: 6  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens  
<400> SEQUENCE: 12  
Gly Pro Gly Met Asp Val  
1 . . . 5

<210> SEQ ID NO 13  
<211> LENGTH: 63  
<212> TYPE: DNA  
<213> ORGANISM: artificial sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: linker  
<220> FEATURE:  
<221> NAME/KEY: CDS



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<210> SEQ ID NO 18  
<211> LENGTH: 34  
<212> TYPE: DNA  
<213> ORGANISM: Artificial sequence /primer  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(34)  
<223> OTHER INFORMATION: PCR primer  
<400> SEQUENCE: 18  
tcctcagcgc gcggctctgg tggcagaccg aagg 34

<210> SEQ ID NO 19  
<211> LENGTH: 33  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(33)  
<223> OTHER INFORMATION: Sequence derived from AF237583 GenBank acc. number  
<400> SEQUENCE: 19  
caggcggcgc gcgggcagcc ccaggaacca cag 33

<210> SEQ ID NO 20  
<211> LENGTH: 94  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(94)  
<223> OTHER INFORMATION: Sequence derived from AF237583 GenBank acc. number  
<400> SEQUENCE: 20  
acgtcgatcg cctgctgaat tcttaagtac tatccaggcc cagcagtggg tttgggattg 60  
gttgccact agtttaccc gggacaggg agag 94

<210> SEQ ID NO 21  
<211> LENGTH: 41  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(41)  
<223> OTHER INFORMATION: Sequence derived from AF237583 GenBank acc. number  
<400> SEQUENCE: 21  
aggcggcgcg cgacaaaact cacacatgcc caccgtgcc a 41

<210> SEQ ID NO 22  
<211> LENGTH: 33  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(33)  
<223> OTHER INFORMATION: Sequence derived from J00220 GenBank acc. number  
<400> SEQUENCE: 22  
caggcggcgc gcgttccctc aactccacct acc 33

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<210> SEQ ID NO 23  
<211> LENGTH: 32  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(32)  
<223> OTHER INFORMATION: Sequence derived from J00220 GenBank acc. number  
<400> SEQUENCE: 23  
ccgctactag ttttacccgc caaggctcg at 32

<210> SEQ ID NO 24  
<211> LENGTH: 31  
<212> TYPE: DNA  
<213> ORGANISM: Mus musculus  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(31)  
<223> OTHER INFORMATION: Sequence derived from L27437 GenBank acc. number  
<400> SEQUENCE: 24  
caggcggcgc gccggcagacc gaaggctcca c 31

<210> SEQ ID NO 25  
<211> LENGTH: 32  
<212> TYPE: DNA  
<213> ORGANISM: Mus musculus  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(32)  
<223> OTHER INFORMATION: Sequence derived from J00220 GenBank acc. number  
<400> SEQUENCE: 25  
ccgctactag ttttaccagg agagtggag ag 32

<210> SEQ ID NO 26  
<211> LENGTH: 36  
<212> TYPE: DNA  
<213> ORGANISM: Mus musculus  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(36)  
<223> OTHER INFORMATION: Sequence derived from L27437 GenBank acc. number  
<400> SEQUENCE: 26  
caggcggcgc gcgggtgtaa gccttgata tgtaca 36

<210> SEQ ID NO 27  
<211> LENGTH: 33  
<212> TYPE: DNA  
<213> ORGANISM: Rattus norvegicus  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(33)  
<223> OTHER INFORMATION: Sequence derived from M28671 GenBank acc. number  
<400> SEQUENCE: 27  
caggcggcgc gcgggtgtat cagaaaacca cag 33

<210> SEQ ID NO 28  
<211> LENGTH: 33  
<212> TYPE: DNA

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<213> ORGANISM: Rattus norvegicus  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(33)  
<223> OTHER INFORMATION: Sequence derived from M28671 GenBank acc. number  
<400> SEQUENCE: 28  
ccgctactag ttttacccgg aggccgggag atg 33

<210> SEQ ID NO 29  
<211> LENGTH: 33  
<212> TYPE: DNA  
<213> ORGANISM: Rattus norvegicus  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(33)  
<223> OTHER INFORMATION: Sequence derived from M28671 GenBank acc. number  
<400> SEQUENCE: 29  
caggcggcgc gccacaaaatg ccctacatgc cct 33

<210> SEQ ID NO 30  
<211> LENGTH: 35  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(35)  
<223> OTHER INFORMATION: Universal oligonucleotide for VL1 amplification.  
<400> SEQUENCE: 30  
caggttgca ctcggacatc crgdtgaccc agtct 35

<210> SEQ ID NO 31  
<211> LENGTH: 35  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(35)  
<223> OTHER INFORMATION: nucleotide in position 29 is "n"  
Universal oligonucleotide for VL2 amplification.  
<400> SEQUENCE: 31  
caggttgca ctcggatatt gtgwtgacac agwct 35

<210> SEQ ID NO 32  
<211> LENGTH: 31  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(31)  
<223> OTHER INFORMATION: Universal oligonucleotide for VL3 amplification.  
<400> SEQUENCE: 32  
caggttgca ctcgcagcct gtgctgcary c 31

<210> SEQ ID NO 33  
<211> LENGTH: 35  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:

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<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(35)  
<223> OTHER INFORMATION: Universal oligonucleotide for VL4 amplification.  
<400> SEQUENCE: 33  
caggtgtgca ctcgtcctat gwgctgacwc agcca 35

<210> SEQ ID NO 34  
<211> LENGTH: 29  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(29)  
<223> OTHER INFORMATION: Universal oligonucleotide for JH1 amplification.  
<400> SEQUENCE: 34  
gaccgcgcg cgaggacrgt gaccagggt 29

<210> SEQ ID NO 35  
<211> LENGTH: 29  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc\_feature  
<222> LOCATION: (1)..(29)  
<223> OTHER INFORMATION: Universal oligonucleotide for JH2 amplification.  
<400> SEQUENCE: 35  
gaccgcgcg cagagacggt gaccrtkgt 29

<210> SEQ ID NO 36  
<211> LENGTH: 5  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens  
<400> SEQUENCE: 36  
Lys Ser Ser Lys Cys  
1 5

<210> SEQ ID NO 37  
<211> LENGTH: 6  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens  
<400> SEQUENCE: 37  
Leu Gly Arg Leu His Met  
1 5